



SEQUENCE LISTING

<110> Labas, Yulii Aleksandrovich
Gurskaya, Nadezda Georgievna
Yanushevich, Yuriy
Fradkov, Arcady Fedorovich
Lukyanov, Konstantin
Lukyanov, Sergey
Matz, Mikhail Vladimirovich

<120> NOVEL CHROMOPHORES/FLUOROPHORES AND
METHODS FOR USING THE SAME

<130> CLON-090

<140> 10/757,356

<141> 2004-01-13

<150> 60/332,980

<151> 2001-11-13

<150> PCT/US02/36499

<151> 2002-11-12

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 868

<212> DNA

<213> Heteractis crispa

<400> 1

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aac gacc aca	act tca agt g	ca ct gca ga a	gg aaa agg ag	aacc ataca a	agg ct caca a	180
ag cct gac ga	tc acc gta ac	tga agg aggt	cct ct gcc at	tt gc ctt cga	ca tt ctt tca	240
ca cgc ctt tc	ga ta tgg caa	ta aggt gtt c	gcc aag tacc	cca aag at ca	tc ct ga ttt t	300
tt ta agc agt	ct ctt cct ga	agg ttt tact	tgg gaa agag	ta ag ca act a	tg agg acg ga	360
gg agt cct ta	cc gtt aaaca	aga aact agt	ct gg agg gag	att gc att at	tt gcaaaa att	420
aa agcac atg	gc act aact t	ccc gc agat	gg tcc ggt ga	tg caaaa acg	ga ccaaat gga	480
tgg gag ccat	ca act gaa ac	ggt tattcca	cgg ggt ggag	ga att ct gat	gc gc gat gtg	540
ccc gcact ga	ag ct gct tgg	ta acaaa gga	ca tct tct ct	gc gt cat gga	aaca act tac	600
aag tcaaaaa	aaaa aggt ga	ac ct gccaaa	cc gc act ttc	at cattt gag	aat gg aga ag	660
ga tagt gtta	gt gac gat ga	ga ag acc att	gag cag cacg	aga at gt gag	gg ca ag ct ac	720
tt caat gata	gt ggaaa atg	at cattt cct	tatt gat ttc	aat gtt aggg	ca tt cag ttt	780
cca aatt ttc	ttag acac ag	tct ttt cct t	tag ctt cgt a	gc ct act tac	cc atg tttt g	840
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<211> 225

<212> PRT

<213> Heteractis crispa

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			20					25					30		
Glu	Pro	Tyr	Lys	Gly	Ser	Gln	Ser	Leu	Thr	Ile	Thr	Val	Thr	Glu	Gly
		35					40					45			
Gly	Pro	Leu	Pro	Phe	Ala	Phe	Asp	Ile	Leu	Ser	His	Ala	Phe	Arg	Tyr
	50					55					60				
Gly	Asn	Lys	Val	Phe	Ala	Lys	Tyr	Pro	Lys	Asp	His	Pro	Asp	Phe	Phe
65					70					75					80
Lys	Gln	Ser	Leu	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Val	Ser	Asn	Tyr
			85						90					95	
Glu	Asp	Gly	Gly	Val	Leu	Thr	Val	Lys	Gln	Glu	Thr	Ser	Leu	Glu	Gly
		100						105					110		
Asp	Cys	Ile	Ile	Cys	Lys	Ile	Lys	Ala	His	Gly	Thr	Asn	Phe	Pro	Ala
	115						120					125			
Asp	Gly	Pro	Val	Met	Gln	Lys	Arg	Thr	Asn	Gly	Trp	Glu	Pro	Ser	Thr
	130					135					140				
Glu	Thr	Val	Ile	Pro	Arg	Gly	Gly	Gly	Ile	Leu	Met	Arg	Asp	Val	Pro
145					150					155					160
Ala	Leu	Lys	Leu	Leu	Gly	Asn	Lys	Gly	His	Leu	Leu	Cys	Val	Met	Glu
				165					170					175	
Thr	Thr	Tyr	Lys	Ser	Lys	Lys	Lys	Gly	Glu	Pro	Ala	Lys	Pro	His	Phe
			180					185					190		
His	His	Leu	Arg	Met	Glu	Lys	Asp	Ser	Val	Ser	Asp	Asp	Glu	Lys	Thr
		195					200					205			
Ile	Glu	Gln	His	Glu	Asn	Val	Arg	Ala	Ser	Tyr	Phe	Asn	Asp	Ser	Gly
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Lys															
225															

<210> 3
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 <212> DNA
 <213> Dendronephthya sp

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 attgaagggg aaggaaaagg aaggccctac gaagggacac agaccttgaa cctgacagtg 180
 aaagaaggcg cgctctccc attttcttac gacatcttga caacagcatt gcactacgga 240
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 gaaggatatt cctgggaaag aaccatgact tatgaagaca agggcatttg taccatcaga 360
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 tttccccc aa atggtccagt tatgcagaag aaaactttga agtggaacc atccacagag 480
 aagctgcacg tgcgtgatgg gttgctgtgc ggtaatatta acatggctct gctgcttgaa 540
 ggaggtggac attacctgtg tgacttcaaa actacttaca aagcgaagaa ggttgttcag 600
 ttgccagatt atcattttgt ggaccatcgc attgagatct tgagtaatga cagcgattac 660
 aacaaagtga agctgtacga gcatggggtt gctcgtatt ctccgttgcc caagtcaggc 720
 ctggtagagg ttcaaggga agccataatg actgcataga taaacatgta gtgaagacca 780
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 ttggg 845

<210> 4
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 <212> PRT
 <213> Dendronephthya sp

<400> 4

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Asn	Val	Asn	Gly	His	Ala	Phe	Val	Ile	Glu	Gly	Glu	Gly	Lys	Gly	Arg
			20					25					30		
Pro	Tyr	Glu	Gly	Thr	Gln	Thr	Leu	Asn	Leu	Thr	Val	Lys	Glu	Gly	Ala
		35					40					45			
Pro	Leu	Pro	Phe	Ser	Tyr	Asp	Ile	Leu	Thr	Thr	Ala	Leu	His	Tyr	Gly
		50				55					60				
Asn	Arg	Val	Phe	Thr	Glu	Tyr	Pro	Ala	Asp	Ile	Thr	Asp	Tyr	Phe	Lys
65					70					75					80
Gln	Ser	Phe	Pro	Glu	Gly	Tyr	Ser	Trp	Glu	Arg	Thr	Met	Thr	Tyr	Glu
				85					90					95	
Asp	Lys	Gly	Ile	Cys	Thr	Ile	Arg	Ser	Asp	Ile	Ser	Leu	Glu	Gly	Asp
			100					105					110		
Cys	Phe	Phe	Gln	Asn	Ile	Arg	Phe	Asn	Gly	Met	Asn	Phe	Pro	Pro	Asn
		115					120					125			
Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Leu	Lys	Trp	Glu	Pro	Ser	Thr	Glu
		130				135					140				
Lys	Leu	His	Val	Arg	Asp	Gly	Leu	Leu	Val	Gly	Asn	Ile	Asn	Met	Ala
145					150					155					160
Leu	Leu	Leu	Glu	Gly	Gly	Gly	His	Tyr	Leu	Cys	Asp	Phe	Lys	Thr	Thr
				165					170					175	
Tyr	Lys	Ala	Lys	Lys	Val	Val	Gln	Leu	Pro	Asp	Tyr	His	Phe	Val	Asp
			180					185					190		
His	Arg	Ile	Glu	Ile	Leu	Ser	Asn	Asp	Ser	Asp	Tyr	Asn	Lys	Val	Lys
		195					200					205			
Leu	Tyr	Glu	His	Gly	Val	Ala	Arg	Tyr	Ser	Pro	Leu	Pro	Lys	Ser	Gly
	210					215					220				
Leu	Val	Glu	Val	Gln	Gly	Lys	Ala	Ile	Met	Thr	Ala				
225					230					235					

<210> 5

<211> 851

<212> DNA

<213> Zoanthus sp

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tgcgctgatg	gacataagtt	tgtaatcgag	ggcaacggca	atggaaatcc	tttcaaaggg	180
aaacagttta	ttaatctgtg	tgtgattgaa	ggaggaccac	tgccattctc	cgaagacata	240
ttgtctgctg	cgtttgacta	cggaacagg	ctcttactg	aatatcctga	aggcatagtt	300
gactatttca	agaactcgtg	tcctgctgga	tatacgtggc	acaggtcttt	tcgctttgaa	360
gatggagcag	tttgcataatg	cagtgcagat	ataacagtaa	atgttaggga	aaactgcatt	420
tatcatgagt	ccacgtttta	tgagtgaaac	tttctgctg	atggacctgt	gatgaaaaag	480
atgacaacta	attgggaacc	gtcctgcgag	aaaatcatac	caataaatag	tcagaagata	540
ttaaaagggg	atgtctccat	gtacctcctt	ctgaaggatg	gtgggcgtta	ccgctgccag	600
tttgacacaa	tttaciaaagc	aaagactgag	ccaaaagaaa	tgccggactg	gcacttcac	660
cagcataaagc	tcaaccgtga	agaccgcagc	gatgctaaga	atcagaaatg	gcaactgata	720
gaacatgcta	ttgcatcccg	atctgcttta	ccctgataac	aaaggagttg	ctattgcatg	780
tgcatgccta	ttacgctgat	aaaaatgtag	ttttaacatg	caattgtatg	tgcatgcaca	840
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<210> 6

<211> 231

<212> PRT

<213> Zoanthus sp

<400> 6

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Arg	Met	Glu	Gly	Cys	Val	Asp	Gly	His	Lys	Phe	Val	Ile	Glu	Gly	Asn
			20					25					30		
Gly	Asn	Gly	Asn	Pro	Phe	Lys	Gly	Lys	Gln	Phe	Ile	Asn	Leu	Cys	Val
		35					40					45			
Ile	Glu	Gly	Gly	Pro	Leu	Pro	Phe	Ser	Glu	Asp	Ile	Leu	Ser	Ala	Ala
	50					55					60				
Phe	Asp	Tyr	Gly	Asn	Arg	Leu	Phe	Thr	Glu	Tyr	Pro	Glu	Gly	Ile	Val
65				70					75					80	
Asp	Tyr	Phe	Lys	Asn	Ser	Cys	Pro	Ala	Gly	Tyr	Thr	Trp	His	Arg	Ser
			85						90					95	
Phe	Arg	Phe	Glu	Asp	Gly	Ala	Val	Cys	Ile	Cys	Ser	Ala	Asp	Ile	Thr
			100					105					110		
Val	Asn	Val	Arg	Glu	Asn	Cys	Ile	Tyr	His	Glu	Ser	Thr	Phe	Tyr	Gly
		115					120					125			
Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn
	130					135					140				
Trp	Glu	Pro	Ser	Cys	Glu	Lys	Ile	Ile	Pro	Ile	Asn	Ser	Gln	Lys	Ile
145				150						155				160	
Leu	Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg
			165					170					175		
Tyr	Arg	Cys	Gln	Phe	Asp	Thr	Ile	Tyr	Lys	Ala	Lys	Thr	Glu	Pro	Lys
			180					185					190		
Glu	Met	Pro	Asp	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Asn	Arg	Glu	Asp
	195						200					205			
Arg	Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Ile	Glu	His	Ala	Ile
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Ala	Ser	Arg	Ser	Ala	Leu	Pro									
225					230										

<210> 7

<211> 1178

<212> DNA

<213> Scolymia cubensis

<400> 7

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ctaccaacat	gcagcgtgct	gggatgaagg	ttaaggaaca	tatgaagatc	aaactgcgta	180
tgggaggtac	tgtaaacgga	aagcatttcg	cggttaatgg	gacaggagac	ggctaccctt	240
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ttgatatctt	gtcagcagca	ttccagtatg	gcaacagggc	attcaccgaa	taccaacag	360
agatagcaga	ctatttcaag	cagtcgtttg	agtttggcga	ggggttctcc	tggaacgaa	420
gtttcacttt	cgaagatggg	gccatttgcg	tcgccaccaa	cgatataacg	atggttggtg	480
gtgagtttca	gtatgatatt	cgatttgatg	gtctgaactt	ccctgaagat	ggtccagtga	540
tgcaaaagaa	aaccgtaaaa	tgggagccat	ccactgagat	aatgtatatg	caaaatggag	600
tgctgaaggg	tgaggttaac	atggctctgt	tgcttcaaga	caaaagccat	taccgttgcg	660
acctcaaaac	tacttataaa	gctaagaata	atgtgccgca	tcctccaggc	taccactatg	720
tggatcactg	ctattgaaata	ctcgaagaac	gtaaggatca	cgtttaagctg	cgggagcatg	780
ctaaagctcg	ttctagcctg	tcacctacca	gtgcaaaaga	acgaaaggct	taggtgatag	840
tcaaaaagac	aacaagacga	aaatgaaagg	tgttcattgt	tagaatttga	tattttcgat	900
tcaatgattc	gttaagggat	ttgctagagg	ctagctaaca	ggttaacatc	ataaggatag	960

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agattycgtt gcggagttag aaccttwata ttttccgaat tccamctaga gtcgttgaga 1020
aatttattag agactagctt tagagttact tttgtggaaa aaaagggttc cattttttgc 1080
gttattacag catttaaagc ataggaatag agattcggtt atggaaaata acagtaggaa 1140
aatacgttgt gaaaataaac ttgttgctga aaaaaaaa 1178

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<210> 8
 <211> 234
 <212> PRT
 <213> Scolymia cubensis

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Arg Met Gly Gly Thr Val Asn Gly Lys His Phe Ala Val Asn Gly Thr
 20          25          30
Gly Asp Gly Tyr Pro Tyr Gln Gly Lys Gln Ile Leu Lys Leu Ile Val
 35          40          45
Glu Gly Ser Glu Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Ala Ala
 50          55          60
Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Thr Glu Ile Ala
 65          70          75          80
Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Ser Trp Glu
 85          90          95
Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr Asn Asp
100          105          110
Ile Thr Met Val Gly Gly Glu Phe Gln Tyr Asp Ile Arg Phe Asp Gly
115          120          125
Leu Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr Val Lys
130          135          140
Trp Glu Pro Ser Thr Glu Ile Met Tyr Met Gln Asn Gly Val Leu Lys
145          150          155          160
Gly Glu Val Asn Met Ala Leu Leu Leu Gln Asp Lys Ser His Tyr Arg
165          170          175
Cys Asp Leu Lys Thr Thr Tyr Lys Ala Lys Asn Asn Val Pro His Pro
180          185          190
Pro Gly Tyr His Tyr Val Asp His Cys Ile Glu Ile Leu Glu Glu Arg
195          200          205
Lys Asp His Val Lys Leu Arg Glu His Ala Lys Ala Arg Ser Ser Leu
210          215          220
Ser Pro Thr Ser Ala Lys Glu Arg Lys Ala
225          230

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<210> 9
 <211> 819
 <212> DNA
 <213> Scolymia cubensis

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gatcacactg cgtatggacg gtgctgtaaa cggaagccc ttcgcggtta atggaacagg 180
agatggcaac ccttatggtg gaatacagag tttgaagctt accgtcgatg gcaacaaacc 240
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cgaataccca aaagagatat cagactatct caagcagtcg tttgagtttg gcgagggggt 360
tacctgggaa cgaagtttca ctttcgaaga cggggccatt tgcgtcgcca cgaacgatat 420
aaagatgggt ggcgatgagt ttcaatataa cattcgattt gatggtgtga atttccctga 480
agatggtccw gtyatgcaga agaaaacggt gaagtgggag ccatccacag agataatgcg 540

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tgtgcaaggt ggagtgctaa aggggtgaggt taacatggct ctgttgctta aagacaaaag 600
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gcttccagac taccactatg tggatcactg tattgaaatc accgaggaaa atagggatta 720
cgттаagctg caggagtatg ctaaagctcg ttctggcctg cacctgcccg aactgcaaaa 780
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<210> 10
 <211> 235
 <212> PRT
 <213> *Scolymia cubensis*

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20     25     30
Gly Thr Gly Asp Gly Asn Pro Tyr Gly Gly Ile Gln Ser Leu Lys Leu
35     40     45
Thr Val Asp Gly Asn Lys Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser
50     55     60
Ala Ala Phe Gln Tyr Gly Asn Arg Ala Phe Thr Glu Tyr Pro Lys Glu
65     70     75     80
Ile Ser Asp Tyr Phe Lys Gln Ser Phe Glu Phe Gly Glu Gly Phe Thr
85     90     95
Trp Glu Arg Ser Phe Thr Phe Glu Asp Gly Ala Ile Cys Val Ala Thr
100    105    110
Asn Asp Ile Lys Met Val Gly Asp Glu Phe Gln Tyr Asn Ile Arg Phe
115    120    125
Asp Gly Val Asn Phe Pro Glu Asp Gly Pro Val Met Gln Lys Lys Thr
130    135    140
Val Lys Trp Glu Pro Ser Thr Glu Ile Met Arg Val Gln Gly Gly Val
145    150    155    160
Leu Lys Gly Glu Val Asn Met Ala Leu Leu Lys Asp Lys Ser His
165    170    175
Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Lys Ala Lys Asn Pro Val Pro
180    185    190
Pro Thr Ala Leu Pro Asp Tyr His Tyr Val Asp His Cys Ile Glu Ile
195    200    205
Thr Glu Glu Asn Arg Asp Tyr Val Lys Leu Gln Glu Tyr Ala Lys Ala
210    215    220
Arg Ser Gly Leu His Leu Pro Glu Leu Gln Lys
225    230    235

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<210> 11
 <211> 807
 <212> DNA
 <213> *Ricordea florida*

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gaaaaggcaa accctatgag ggatcgagcagg aattaaccct tgccgtggtg gaaggagggc 180
ctctgccttt ctcttatgat atcctgacaa cgatagttca ctatggcaac agggcatttg 240
tgaactaccc aaaggacata ccagatattt tcaagcagac ctgctctggt cctgggtgctg 300
gatattcctg gcaaaggacc atgagttttg aagacggagg cgtttgact gctacgagcc 360
atatcagggt ggatggcgac actttcaatt atgacattca cttcatggga gcggatttcc 420
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caggttacca ttttgtggac cactgcattg agataacgag tcaacaggac gattacaacg 660
tggttgagct gtacgagggg gctgtagccc actactctcc tctgcagaaa ccattgccaag 720
caaaggcata aagccaaaca acccaagagg acaacaagac atttaatcaa atcacatctt 780
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<210> 12
 <211> 231
 <212> PRT
 <213> Ricordea florida

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20     25     30
Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Ala Val Val Glu Gly Gly
35     40     45
Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Thr Ile Val His Tyr Gly
50     55     60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65     70     75     80
Gln Thr Cys Ser Gly Pro Gly Ala Gly Tyr Ser Trp Gln Arg Thr Met
85     90     95
Ser Phe Glu Asp Gly Gly Val Cys Thr Ala Thr Ser His Ile Arg Val
100    105    110
Asp Gly Asp Thr Phe Asn Tyr Asp Ile His Phe Met Gly Ala Asp Phe
115    120    125
Pro Leu Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
130    135    140
Ser Thr Glu Ile Met Phe Gln Cys Asp Gly Leu Leu Arg Gly Asp Val
145    150    155    160
Ala Met Ser Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe
165    170    175
Lys Thr Ile Tyr Lys Pro Lys Lys Asn Val Lys Met Pro Gly Tyr His
180    185    190
Phe Val Asp His Cys Ile Glu Ile Thr Ser Gln Gln Asp Asp Tyr Asn
195    200    205
Val Val Glu Leu Tyr Glu Gly Ala Val Ala His Tyr Ser Pro Leu Gln
210    215    220
Lys Pro Cys Gln Ala Lys Ala
225    230

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<210> 13
 <211> 796
 <212> DNA
 <213> Ricordea florida

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<400> 13
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taaaatgggt ggcgttggtta acgggcagtc atttcagatc gatggggaag gaaaaggcaa 180
accttacgag ggatcacaga aattaaccct tgaagtgggt gaaggagggc ctctgctctt 240
ctcttatgat atcctgacaa cgatatttca gtatggcaac agggcattcg tgaactaccc 300
aaaggacata ccagatattt tcaagcagac ctgctctggt cctgatgggt gattttcctg 360
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tgatggattg ctgaggggtg acattgccat gtctctgttg ctgaaaggag gcggccatta 600
ccgatgtgac tttaaaacta tttatacacc caagaggaag gtcaacatgc caggttacca 660
ttttgtggac cactgcattg agatacagaa gcacgacaag gattacaaca tggctgtgct 720
ctctgaggat gctgtagccc acaactctcc tctggagaaa aaaagccaag caaaggcgta 780
aagccaaaca acctaa 796

```

<210> 14
 <211> 231
 <212> PRT
 <213> Ricordea florida

```

<400> 14
Met Ser Ala Leu Lys Glu Glu Met Lys Ile Lys Leu Lys Met Val Gly
1      5      10      15
Val Val Asn Gly Gln Ser Phe Gln Ile Asp Gly Glu Gly Lys Gly Lys
20     25     30
Pro Tyr Glu Gly Ser Gln Lys Leu Thr Leu Glu Val Val Glu Gly Gly
35     40     45
Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
50     55     60
Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
65     70     75     80
Gln Thr Cys Ser Gly Pro Asp Gly Gly Phe Ser Trp Gln Arg Thr Met
85     90     95
Thr Tyr Glu Asp Gly Gly Val Cys Thr Ala Ser Asn His Ile Ser Val
100    105    110
Asp Gly Asp Thr Phe Tyr Tyr Val Ile Arg Phe Asn Gly Glu Asn Phe
115    120    125
Pro Pro Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
130    135    140
Ser Thr Glu Ile Met Phe Glu Arg Asp Gly Leu Leu Arg Gly Asp Ile
145    150    155    160
Ala Met Ser Leu Leu Lys Gly Gly Gly His Tyr Arg Cys Asp Phe
165    170    175
Lys Thr Ile Tyr Thr Pro Lys Arg Lys Val Asn Met Pro Gly Tyr His
180    185    190
Phe Val Asp His Cys Ile Glu Ile Gln Lys His Asp Lys Asp Tyr Asn
195    200    205
Met Ala Val Leu Ser Glu Asp Ala Val Ala His Asn Ser Pro Leu Glu
210    215    220
Lys Lys Ser Gln Ala Lys Ala
225    230

```

<210> 15
 <211> 795
 <212> DNA
 <213> Montastraea cavernosa

```

<400> 15
acgcagggat tcaccctggt gatttggaa agagcagacc gagaacaaca agagctgtat 60
aaggctgata tcttacttta cgtctacat catgagtgtg attaaatcag tcatgaagat 120
caagctgcgt atggaaggca gtgtaaacgg gcacaacttc gtaattgttg gagaaggaga 180
aggcaagcct tatgagggaa cacagagtat ggaccttaca gtcaaagaag gcgcacctct 240
gcctttcgcc tacgatatca tgacaacagt attccattac ggcaataggg tattcgcaaa 300
atacccaaaa catatcccag actatttcaa gcagatgttt cctgaggagt attcctggga 360

```



```

acgaagcatg aatttcgaag gcgggggcat ttgcaccgcc aggaacgaga taacaatgga 420
aggcgactgt tttttcaata aagttcgatt tgatggtgtg aacttcccc ccaatggtcc 480
agtcattgcag aagaagacgc tgaatggga gccatccact gaaaaaatgt atgtgctga 540
tgagtgctg acgggtgata tcaacatggc tttgttgctt gaaggagggt gccattaccg 600
atgtgacttc agaactactt acagagctaa gaagaagggt gtcaagttac cagattatca 660
ctttgaggat cactccattg agattttgcg ccatgacaaa gaatacactg aggttaagct 720
gtatgagcat gccgaagctc attctgggct gccgagggtg gcaaagtaaa ggcttaacga 780
aaagccaaga ccaca 795

```

<210> 16

<211> 235

<212> PRT

<213> Montastraea cavernosa

<400> 16

```

Arg Leu Ile Ser Tyr Phe Thr Ser Thr Ile Met Ser Val Ile Lys Ser
1      5      10      15
Val Met Lys Ile Lys Leu Arg Met Glu Gly Ser Val Asn Gly His Asn
20     25     30
Phe Val Ile Val Gly Glu Gly Glu Gly Lys Pro Tyr Glu Gly Thr Gln
35     40     45
Ser Met Asp Leu Thr Val Lys Glu Gly Ala Pro Leu Pro Phe Ala Tyr
50     55     60
Asp Ile Met Thr Thr Val Phe His Tyr Gly Asn Arg Val Phe Ala Lys
65     70     75     80
Tyr Pro Lys His Ile Pro Asp Tyr Phe Lys Gln Met Phe Pro Glu Glu
85     90     95
Tyr Ser Trp Glu Arg Ser Met Asn Phe Glu Gly Gly Gly Ile Cys Thr
100    105    110
Ala Arg Asn Glu Ile Thr Met Glu Gly Asp Cys Phe Phe Asn Lys Val
115    120    125
Arg Phe Asp Gly Val Asn Phe Pro Pro Asn Gly Pro Val Met Gln Lys
130    135    140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Val Arg Asp
145    150    155    160
Gly Val Leu Thr Gly Asp Ile Asn Met Ala Leu Leu Leu Glu Gly Gly
165    170    175
Gly His Tyr Arg Cys Asp Phe Arg Thr Thr Tyr Arg Ala Lys Lys Lys
180    185    190
Gly Val Lys Leu Pro Asp Tyr His Phe Glu Asp His Ser Ile Glu Ile
195    200    205
Leu Arg His Asp Lys Glu Tyr Thr Glu Val Lys Leu Tyr Glu His Ala
210    215    220
Glu Ala His Ser Gly Leu Pro Arg Val Ala Lys
225    230    235

```

<210> 17

<211> 1066

<212> DNA

<213> Montastraea cavernosa

<400> 17

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attcgccctg gtgatttggga agagagcaga tcgagaacaa caagagctgt aaggttgata 60
tcttacttac gtctaccatc atgacaagtg ttgcacagga aaagggtgtg attaaaccag 120
acatgaagat gaagctgcgt atggaagggt ctgtaaacgg gcacaagttc gtggttgaaag 180
gagatggaaa agggaagcct ttcgacggaa cacagactat ggaccttaca gtcatagaag 240
gcgcaccatt gcctttcgct tacgatatct tgacaacagt attcgattac ggcaacaggg 300

```

```

tattcgccaa atacccagaa gacatagcag attatttcaa gcagacgttt cctgaggggt 360
acttctggga acgaagcatg acatacgaag accagggcat ttgcatcgcc acaaacgaca 420
taacaatgat ggaaggcgtc gacgactgtt ttgcctataa aattcgattt gatggtgtga 480
actttcctgc caatggtcca gttatgcaga ggaagacgct gaaatgggag ccatccactg 540
agataatgta tgcgcgtgat ggagtgcgtg aggggtgatgt taacatggct ctgttgcttg 600
aaggaggtgg ccattaccga tgtgacttca aaactactta caaagctaag aaggttgtcc 660
ggttgccaga ctatcacttt gtggaccatc gcattgagat tgtgagccac gacaaagatt 720
acaacaaggc taagctgcac gagcatgccg aagctcgtca tggactgtca aggaaggcca 780
agtaaaggct taatgaaaag tcaagacgac aacgaggaga aacaaagtac ttttttgta 840
aatttgaagg catttactcg gaattagtat ttgatacttt cgattcaagg atttgttccg 900
ggatttgta gagactagct ctagagtgtt attttgtgaa aaaagatagt ttccagtttt 960
tgcgggatta cagcatgggg atagactttt taaactcagt tgttgtcaaa tgcaagtaag 1020
aaaactgtag tgagaataaa cttgttatcg aagccgaaaa aaaaaa 1066

```

<210> 18

<211> 234

<212> PRT

<213> Montastraea cavernosa

<400> 18

```

Met Thr Ser Val Ala Gln Glu Lys Gly Val Ile Lys Pro Asp Met Lys
 1          5          10          15
Met Lys Leu Arg Met Glu Gly Ala Val Asn Gly His Lys Phe Val Val
          20          25          30
Glu Gly Asp Gly Lys Gly Lys Pro Phe Asp Gly Thr Gln Thr Met Asp
          35          40          45
Leu Thr Val Ile Glu Gly Ala Pro Leu Pro Phe Ala Tyr Asp Ile Leu
          50          55          60
Thr Thr Val Phe Asp Tyr Gly Asn Arg Val Phe Ala Lys Tyr Pro Glu
65          70          75          80
Asp Ile Ala Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr Phe Trp
          85          90          95
Glu Arg Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Ile Ala Thr Asn
          100          105          110
Asp Ile Thr Met Met Glu Gly Val Asp Asp Cys Phe Ala Tyr Lys Ile
          115          120          125
Arg Phe Asp Gly Val Asn Phe Pro Ala Asn Gly Pro Val Met Gln Arg
          130          135          140
Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Ile Met Tyr Ala Arg Asp
145          150          155          160
Gly Val Leu Lys Gly Asp Val Asn Met Ala Leu Leu Leu Glu Gly Gly
          165          170          175
Gly His Tyr Arg Cys Asp Phe Lys Thr Thr Tyr Lys Ala Lys Lys Val
          180          185          190
Val Arg Leu Pro Asp Tyr His Phe Val Asp His Arg Ile Glu Ile Val
          195          200          205
Ser His Asp Lys Asp Tyr Asn Lys Val Lys Leu His Glu His Ala Glu
210          215          220
Ala Arg His Gly Leu Ser Arg Lys Ala Lys
225          230

```

<210> 19

<211> 898

<212> DNA

<213> Condylactis gigantea

<400> 19

```

acagctgttc atccacgctc attcaagacg ccgtaactt tattccagtc aggaaaatgt 60
atccttggat caaggaaacc atgcgcagta aggtttacat ggaaggagat gttacaacc 120
acgccttcaa gtgcactgca gtaggagaag gaaaaccata caaaggctca caagacctga 180
cgattaccgt cactgaagga ggtcctctgc catttgcttt cgacattctt tcacacgcct 240
ttcagtatgg caacaagggtg ttcaccgatt accccgacga tattcctgat ttctttaagc 300
agtctctctc ggatgggtttt acttgagaa gagtaagcac statgacgat ggaggagtcc 360
tcacagttac ccaagacact agtctgaagg gagattgcat tatttgcaac attaaagtcc 420
atggcactaa cttccccgaa aatgggtccg tgatgcaaaa caagaccgat ggatgggagc 480
catccagcac tgaaacggtt attccacaag atggaggaat tgttgctgcg cgatcaccgc 540
cactaaggct gcgtgataaa ggtcatctta tctgccacat ggaaacaact tacaagccaa 600
acaaagaggt gaagctgcc gaactccact ttcattcatt gcgaatggaa aagctgagt 660
ttagtgacga tgggaagacc attaaagcag acgagtatgt ggtggctagc tactccaaag 720
tgccttcgaa gataggacgt caatgatcat ttcccttatt aaatatcaat gatgtggctt 780
tcaattttcc aaaattttgt taagacatag gtcttttgga tttttgtaa ccccaacctt 840
aattcccaat aatttttgtt ggaaagtcaa ataaaaccag ccttccttgc gcctttaa 898

```

<210> 20

<211> 229

<212> PRT

<213> *Condylactis gigantea*

<400> 20

```

Met Tyr Pro Trp Ile Lys Glu Thr Met Arg Ser Lys Val Tyr Met Glu
 1           5           10           15
Gly Asp Val Asn Asn His Ala Phe Lys Cys Thr Ala Val Gly Glu Gly
          20           25           30
Lys Pro Tyr Lys Gly Ser Gln Asp Leu Thr Ile Thr Val Thr Glu Gly
          35           40           45
Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser His Ala Phe Gln Tyr
          50           55           60
Gly Asn Lys Val Phe Thr Asp Tyr Pro Asp Asp Ile Pro Asp Phe Phe
65          70          75          80
Lys Gln Ser Leu Ser Asp Gly Phe Thr Trp Arg Arg Val Ser Thr Tyr
          85          90          95
Asp Asp Gly Gly Val Leu Thr Val Thr Gln Asp Thr Ser Leu Lys Gly
          100          105          110
Asp Cys Ile Ile Cys Asn Ile Lys Val His Gly Thr Asn Phe Pro Glu
          115          120          125
Asn Gly Pro Val Met Gln Asn Lys Thr Asp Gly Trp Glu Pro Ser Ser
          130          135          140
Thr Glu Thr Val Ile Pro Gln Asp Gly Gly Ile Val Ala Ala Arg Ser
145          150          155          160
Pro Ala Leu Arg Leu Arg Asp Lys Gly His Leu Ile Cys His Met Glu
          165          170          175
Thr Thr Tyr Lys Pro Asn Lys Glu Val Lys Leu Pro Glu Leu His Phe
          180          185          190
His His Leu Arg Met Glu Lys Leu Ser Val Ser Asp Asp Gly Lys Thr
          195          200          205
Ile Lys Gln His Glu Tyr Val Val Ala Ser Tyr Ser Lys Val Pro Ser
210          215          220
Lys Ile Gly Arg Gln
225

```

<210> 21

<211> 1030

<212> DNA

<213> *Agaricia fragilis*

<400> 21

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caaggaagcc aaatctttta ccagagatct cgcgtgaaag caacctatga gtgatggcga 60
tttctactct aaagaacgtc atcatcatcg ttattatata ctctgcagc acttgtgctg 120
tttggtcgaa ttcaaactct gaatcctctt tcactaatgg gattgcagag gaaatgaaga 180
ctagggtaca tttggagggt actgttaacg ggcactcctt tacaattaaa ggcgaaggaa 240
gaggctaccc ttacaaagga gaacagttta tgagccttga ggtcgtcaat ggtgctcctc 300
tgccgtttct ttttgatata ttgacaccag catttatgta tggcaacaga gtgttcacca 360
agtaccaccc aaacatacca gactatttca agcagacggt tcctgaaggg tatcactggg 420
aaagaaacat tccctttgaa gatcaggccg cgtgcacggt aaccagccac ataagattgg 480
aagaggaaga gaggcgtttt gtaaataacg tcagatttca ctgtgtgaac tttcccccta 540
atggtccagt catgcagagg aggatactga aatgggagcc atccactgag aacattttatc 600
cgcgtgatgg gtttctggag ggccatgttg atatgactct tcgggttgaa ggaggtggct 660
attaccgagc tgagttcaaa agtacttaca aagggaagac cccagtcgcg gacatgccag 720
actttcactt catagaccac cgcattgaga ttacggagca tgacgaagac tacaccaatg 780
ttgagctgca tgacgtatcc tgggctcggt actctatgct gccgactatg taagcggaaa 840
aggcaaggca acaagacgca aaaccgccct gtttgcctct tttcataaga gatttgacaa 900
ccgtggttct ttgccattta atttgaatta gtttaaatta aatctttggg attgatgtag 960
acgctttggg tgctaagtaa gaaaacattt gtgattatta aatttggtgc ctgaagcaaa 1020
aaaaaaaaa 1030
```

<210> 22

<211> 259

<212> PRT

<213> *Agaricia fragilis*

<400> 22

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Met Ala Ile Ser Thr Leu Lys Asn Val Ile Ile Ile Val Ile Ile Tyr
 1          5          10          15
Ser Cys Ser Thr Cys Ala Val Trp Ser Asn Ser Asn Ser Glu Ser Ser
 20          25          30
Phe Thr Asn Gly Ile Ala Glu Glu Met Lys Thr Arg Val His Leu Glu
 35          40          45
Gly Thr Val Asn Gly His Ser Phe Thr Ile Lys Gly Glu Gly Arg Gly
 50          55          60
Tyr Pro Tyr Lys Gly Glu Gln Phe Met Ser Leu Glu Val Val Asn Gly
 65          70          75          80
Ala Pro Leu Pro Phe Ser Phe Asp Ile Leu Thr Pro Ala Phe Met Tyr
 85          90          95
Gly Asn Arg Val Phe Thr Lys Tyr Pro Pro Asn Ile Pro Asp Tyr Phe
100          105          110
Lys Gln Thr Phe Pro Glu Gly Tyr His Trp Glu Arg Asn Ile Pro Phe
115          120          125
Glu Asp Gln Ala Ala Cys Thr Val Thr Ser His Ile Arg Leu Glu Glu
130          135          140
Glu Glu Arg Arg Phe Val Asn Asn Val Arg Phe His Cys Val Asn Phe
145          150          155          160
Pro Pro Asn Gly Pro Val Met Gln Arg Arg Ile Leu Lys Trp Glu Pro
165          170          175
Ser Thr Glu Asn Ile Tyr Pro Arg Asp Gly Phe Leu Glu Gly His Val
180          185          190
Asp Met Thr Leu Arg Val Glu Gly Gly Tyr Tyr Arg Ala Glu Phe
195          200          205
Lys Ser Thr Tyr Lys Gly Lys Thr Pro Val Arg Asp Met Pro Asp Phe
210          215          220
His Phe Ile Asp His Arg Ile Glu Ile Thr Glu His Asp Glu Asp Tyr
225          230          235          240
Thr Asn Val Glu Leu His Asp Val Ser Trp Ala Arg Tyr Ser Met Leu
```

Pro Thr Met

245 250 255

<210> 23
 <211> 1024
 <212> DNA
 <213> Ricordea florida

<400> 23
 agccacttcg gtgtcttgtc gagaggaagg atcacgaaca agagaagagc tgtaaaagtt 60
 aaaatttttac tttacttctt ccagcatgaa tgcacttcaa gaggaaatga aaatcaagct 120
 tacaatgggtg ggcgttggtta acgggcagtc atttaagatc gatgggaaag gaaaagggaa 180
 accttacgag ggatcacagg aattgaccct taaagtgggtg gaaggcgggc ctctgctctt 240
 ctcttatgat atcctgacaa cgatatttca gtatggcaac agggcattcg tgaactacc 300
 aaaggacata ccagatatatt tcaagcaaac gtgttctggt cttgatggcg gatattcgtg 360
 gcaaaggacc atgacttatg aggacggagg ggtttgtact gctacaagca acgtcagcgt 420
 ggtcggcgac actttcaatt atgaaattca ctttatgggg gcgaattttc ctccaaatgg 480
 tccrgtgatg cagaaaagaa cagtgaagtg ggagccctcc actgagataa tgtttgaacg 540
 tgatggattg ctgaggggtg atgttcccat gtctctgttg ctgaaaggag gcgaccatta 600
 ccgatgtgac tttaaaacta tttataaacc caacaagaag gtcaagctgc caggttacca 660
 ttttgtggac cactgcattg agataaagag tcaagagaat gattacaaca tggttgcgct 720
 ctttgaggat gctgtagcac actactctcc tctggagaaa aagagccagg caaaggcgta 780
 aatccaaaca acctaagaag acgacaaggc attcaatcta atcgcatgtt tgaatttttg 840
 gttaggaatg tgttgggtca gactaggtct agaacgtttc attttggctg gatttgtttt 900
 actcagttat agacaagaaa aaaatcctaa atgacttggg ttggatttag ctttcggcac 960
 tgtcaattcc ggattcctta gaaatatttg agaccaagcc tttttttgag ctgagaacgt 1020
 aatc 1024

<210> 24
 <211> 231
 <212> PRT
 <213> Ricordea florida

<400> 24
 Met Asn Ala Leu Gln Glu Glu Met Lys Ile Lys Leu Thr Met Val Gly
 1 5 10 15
 Val Val Asn Gly Gln Ser Phe Lys Ile Asp Gly Lys Gly Lys Gly Lys
 20 25 30
 Pro Tyr Glu Gly Ser Gln Glu Leu Thr Leu Lys Val Val Glu Gly Gly
 35 40 45
 Pro Leu Leu Phe Ser Tyr Asp Ile Leu Thr Thr Ile Phe Gln Tyr Gly
 50 55 60
 Asn Arg Ala Phe Val Asn Tyr Pro Lys Asp Ile Pro Asp Ile Phe Lys
 65 70 75 80
 Gln Thr Cys Ser Gly Leu Asp Gly Gly Tyr Ser Trp Gln Arg Thr Met
 85 90 95
 Thr Tyr Glu Asp Gly Gly Val Cys Thr Ala Thr Ser Asn Val Ser Val
 100 105 110
 Val Gly Asp Thr Phe Asn Tyr Glu Ile His Phe Met Gly Ala Asn Phe
 115 120 125
 Pro Pro Asn Gly Pro Val Met Gln Lys Arg Thr Val Lys Trp Glu Pro
 130 135 140
 Ser Thr Glu Ile Met Phe Glu Arg Asp Gly Leu Leu Arg Gly Asp Val
 145 150 155 160
 Pro Met Ser Leu Leu Leu Lys Gly Gly Asp His Tyr Arg Cys Asp Phe
 165 170 175

Lys Thr Ile Tyr Lys Pro Asn Lys Lys Val Lys Leu Pro Gly Tyr His
 180 185 190
 Phe Val Asp His Cys Ile Glu Ile Lys Ser Gln Glu Asn Asp Tyr Asn
 195 200 205
 Met Val Ala Leu Phe Glu Asp Ala Val Ala His Tyr Ser Pro Leu Glu
 210 215 220
 Lys Lys Ser Gln Ala Lys Ala
 225 230

<210> 25
 <211> 913
 <212> DNA
 <213> Montastraea cavernosa

<400> 25
 agagctgttag ggtgatatct tactttacgtc taccatcatg accagtgttg cacaggaaaa 60
 ggggtgtgatt aaaccagaca tgaagatgaa gctgcgtatg gaaggtgctg taaacgggca 120
 caagttcgtg attgaaggag atggaaaagg gaagcctttc gacggaacac agactatgga 180
 ccttacagtc atagaaggcg caccattgcc ttctgcttac gctatcttga caacagtatt 240
 cgattacggc aacagggtat tcgccaaata cccagaagac atagcagatt atttcaagca 300
 gacatttctt gaggggtact tctgggaacg aagcatgaca tacgaagacc agggcatttg 360
 catcgccaca aacgacataa caatgatgaa aggcgtcgac gactgttttg tctataaaat 420
 tcgatttgat ggtgtgaact ttctgccaat tgggtccagt atgcagagga agacgctgaa 480
 atgggagcca tccactgaga aaatgtatgc gcgtgatgga gtgctgaagg gtgatgttaa 540
 catggctctg ttgcttgaag gaggtggcca ttaccgatgt gacttcaaaa ctacttacag 600
 agctaagaag gttgtccagt tgccagacta tcattttgtg gaccatcgca ttgagattgt 660
 gagccacgac aaagattaca acaagggttaa gctgtatgag catgccgaag ctcattcttg 720
 gctgccgagg caggccaagt aaaggcttaa tgaaaagcca agacgacaac aaggagaaac 780
 aaagtatttt tttgtttaa tttcaaggca tttactcgga attagtattt gatactttcg 840
 attcaaggat ttgtttcggg acttggttaga gaccagctct agagttgtat tttgtgaaaa 900
 aaagatagtt tcc 913

<210> 26
 <211> 234
 <212> PRT
 <213> Montastraea cavernosa

<400> 26
 Met Thr Ser Val Ala Gln Glu Lys Gly Val Ile Lys Pro Asp Met Lys
 1 5 10 15
 Met Lys Leu Arg Met Glu Gly Ala Val Asn Gly His Lys Phe Val Ile
 20 25 30
 Glu Gly Asp Gly Lys Gly Lys Pro Phe Asp Gly Thr Gln Thr Met Asp
 35 40 45
 Leu Thr Val Ile Glu Gly Ala Pro Leu Pro Phe Ala Tyr Ala Ile Leu
 50 55 60
 Thr Thr Val Phe Asp Tyr Gly Asn Arg Val Phe Ala Lys Tyr Pro Glu
 65 70 75 80
 Asp Ile Ala Asp Tyr Phe Lys Gln Thr Phe Pro Glu Gly Tyr Phe Trp
 85 90 95
 Glu Arg Ser Met Thr Tyr Glu Asp Gln Gly Ile Cys Ile Ala Thr Asn
 100 105 110
 Asp Ile Thr Met Met Lys Gly Val Asp Asp Cys Phe Val Tyr Lys Ile
 115 120 125
 Arg Phe Asp Gly Val Asn Phe Pro Ala Asn Gly Pro Val Met Gln Arg
 130 135 140
 Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu Lys Met Tyr Ala Arg Asp

145					150					155					160
Gly	Val	Leu	Lys	Gly	Asp	Val	Asn	Met	Ala	Leu	Leu	Leu	Glu	Gly	Gly
				165					170					175	
Gly	His	Tyr	Arg	Cys	Asp	Phe	Lys	Thr	Thr	Tyr	Arg	Ala	Lys	Lys	Val
			180					185					190		
Val	Gln	Leu	Pro	Asp	Tyr	His	Phe	Val	Asp	His	Arg	Ile	Glu	Ile	Val
		195					200					205			
Ser	His	Asp	Lys	Asp	Tyr	Asn	Lys	Val	Lys	Leu	Tyr	Glu	His	Ala	Glu
	210					215					220				
Ala	His	Ser	Gly	Leu	Pro	Arg	Gln	Ala	Lys						
225					230										

<210> 27
 <211> 1133
 <212> DNA
 <213> Montastraea annularis

<400> 27
 tgggttaacgc agagtcgcgg ggggttcctg gctaataatt gattctatatt tgggtgtgac 60
 attcaggttt aaagcagcat cctcagtgct gaggtctcat tcaccctggg gatttggaag 120
 agagcagatc gagaacacca agagctgtat tacgctaaaa tcttacttgc ctctaccacc 180
 atgagtatga ttaaaccaga aatgaagatc aagatgcgta tggacgggtgc tgtaaaccggg 240
 cacaagttcg tgattacagg ggaaggaagc ggcgagcctt tcgagggaaa acagactatg 300
 aacctgacag tcatagacgg cggacctctg cctttcgctt tcgacatctt gacaacagca 360
 ttcgattacg gcamcagggt attcgccaaa taccagaag acatcccaga ctatttcaag 420
 cagtcgtttc ctgagggggt ttcttgggaa cgaagcatga cttacgaaga cgggggcatt 480
 tgcacgcgca caaatgacat aaaaatggaa ggcgactgct tttcctatga aattcgattt 540
 gatgggggtga actttcctgc caatagtcca gttatgcaga agaagaccgt gaaatgggag 600
 ccatgcactg rggaaatgta tgtgcgtgat ggagtgccta aaggtggtct taacatggct 660
 ctgttgcttg aaggaggtgg ccatttccga tgtgacttga aaactactta caaagctaag 720
 aaggttgctc agatgccaga ctatcacttt gtgaatcacc gacttgagat aacatggcat 780
 gacgaggatt acaacaatgt taagctgtct gagcatgcag aagctcattc tggactgccca 840
 aggcaggcca aataaaggct tgacgaaaag ccaaaacggc aaagagtaca agaaagtata 900
 tataaatgta tatttttcaa ctgaaaggca ttccactcgg aattagtatt tgatactttc 960
 aattcaagga tttatttttg gatttgctag ccactagctt tattgttaaa ttaagttaaa 1020
 gacggtttag cattttttcg gtattacaac ataggcacag acgtcttaac cccagtagtg 1080
 gtcaggtaca agtaagaaaa ctttggtgag aatagacttg tagtcgaaaa aaa 1133

<210> 28
 <211> 224
 <212> PRT
 <213> Montastraea annularis

<220>
 <221> VARIANT
 <222> 65, 144
 <223> Xaa = Any Amino Acid

<400> 28
 Met Ser Met Ile Lys Pro Glu Met Lys Ile Lys Met Arg Met Asp Gly
 1 5 10 15
 Ala Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly Ser Gly Glu
 20 25 30
 Pro Phe Glu Gly Lys Gln Thr Met Asn Leu Thr Val Ile Asp Gly Gly
 35 40 45
 Pro Leu Pro Phe Ala Phe Asp Ile Leu Thr Thr Ala Phe Asp Tyr Gly
 50 55 60

Xaa	Arg	Val	Phe	Ala	Lys	Tyr	Pro	Glu	Asp	Ile	Pro	Asp	Tyr	Phe	Lys
65					70					75					80
Gln	Ser	Phe	Pro	Glu	Gly	Phe	Ser	Trp	Glu	Arg	Ser	Met	Thr	Tyr	Glu
				85					90					95	
Asp	Gly	Gly	Ile	Cys	Ile	Ala	Thr	Asn	Asp	Ile	Lys	Met	Glu	Gly	Asp
			100					105					110		
Cys	Phe	Ser	Tyr	Glu	Ile	Arg	Phe	Asp	Gly	Val	Asn	Phe	Pro	Ala	Asn
		115					120					125			
Ser	Pro	Val	Met	Gln	Lys	Lys	Thr	Val	Lys	Trp	Glu	Pro	Cys	Thr	Xaa
	130					135					140				
Glu	Met	Tyr	Val	Arg	Asp	Gly	Val	Leu	Lys	Gly	Gly	Leu	Asn	Met	Ala
145					150					155					160
Leu	Leu	Leu	Glu	Gly	Gly	Gly	His	Phe	Arg	Cys	Asp	Leu	Lys	Thr	Thr
			165						170					175	
Tyr	Lys	Ala	Lys	Lys	Val	Val	Gln	Met	Pro	Asp	Tyr	His	Phe	Val	Asn
		180						185						190	
His	Arg	Leu	Glu	Ile	Thr	Trp	His	Asp	Glu	Asp	Tyr	Asn	Asn	Val	Lys
		195					200					205			
Leu	Ser	Glu	His	Ala	Glu	Ala	His	Ser	Gly	Leu	Pro	Arg	Gln	Ala	Lys
	210					215					220				